==========

Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=6; day=16; hr=14; min=28; sec=40; ms=678;]

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Validated By CRFValidator v 1.0.3

Application No: 10595610 Version No: 1.0

Input Set:

Output Set:

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Finished: 2009-05-28 17:18:50.697
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 532 ms
Total Warnings: 3
Total Errors: 1
No. of SeqIDs Defined: 3
Actual SeqID Count: 3

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W	213	Artificial or Unknown found in <213> in SEQ ID (2)
W	213	Artificial or Unknown found in <213> in SEQ ID (3)

SEQUENCE LISTING

<110> Remer, Ricardo A
Coronha Lima, Marcia
Margis, Rogerio
Alves Ferreira, Marcio

<120> Pharmaceutical Product Comprising Tissue of the Mail Vegetal Reproductive System

<130> 048220.001US

<140> 10595610
<141> 2009-05-28

<150> PCT/BR04/00100
<151> 2004-11-12

<150> BR PI0305197
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<160> 3

<170> PatentIn version 3.5

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<212> DNA
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tatgttctct tttctcatgc cactgttgga ggttattaag attattattg cttctgtggc 180

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taagattatt ataacagctt atattgagat cactcgagat ttatgcttaa ttatataata 480

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ggtggtggag gaagtaaatc caaaagtaaa aaaagtaaac tcaaagctaa attgggaaag 1080

aaaaaaggta tgtccggagg catgtcagga agtgaagaag gtatgtctgg aagtgaagga 1140

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cacaaaattg gaggaggtaa acacggaggt cttggaggta aattcggaaa gaaaagaggc 1500

atgtccggaa gtggaggagg catgtcagga agtgaaggag gtgtgtctgg aagtgaagga 1560

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<211> 543
<212> PRT
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<220>
<223> This protein results from the translation of ATGRP17

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Glu Gly Arg Phe Phe Pro Ser Leu Ser Leu Ser Glu Arg Asp Gly Arg
        35                  40                  45

Lys Phe Ser Phe Leu Ser Met Phe Ser Phe Leu Met Pro Leu Leu Glu
    50                  55                  60

Val Ile Lys Ile Ile Ile Ala Ser Val Ala Ser Val Ile Phe Val Gly
65                  70                  75                  80

Phe Ala Cys Val Thr Leu Ala Gly Ser Ala Ala Ala Leu Val Val Ser
                85                  90                  95

Thr Pro Val Phe Ile Ile Phe Ser Pro Val Leu Val Pro Ala Thr Ile
            100                 105                 110

Ala Thr Val Val Leu Ala Thr Gly Phe Thr Ala Gly Gly Ser Phe Gly
        115                 120                 125

Ala Thr Ala Leu Gly Leu Ile Met Trp Leu Val Lys Arg Arg Met Gly
    130                 135                 140

Val Lys Pro Lys Asp Asn Pro Pro Pro Ala Gly Leu Pro Pro Asn Ser
145                 150                 155                 160

Gly Ala Gly Ala Gly Gly Ala Gln Ser Leu Ile Lys Lys Ser Lys Ala
                165                 170                 175

Lys Ser Lys Gly Gly Leu Lys Ala Trp Cys Lys Lys Met Leu Lys Ser
            180                 185                 190

Lys Phe Gly Gly Lys Lys Gly Lys Ser Gly Gly Gly Lys Ser Lys Phe
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Gly Gly Lys Gly Gly Lys Ser Glu Gly Glu Glu Gly Met Ser Ser Gly
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Asp Glu Gly Met Ser Gly Ser Glu Gly Gly Met Ser Gly Gly Glu Gly
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Gly Lys Ser Lys Ser Gly Lys Gly Lys Leu Lys Ala Lys Leu Glu Lys
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Lys Lys Gly Met Ser Gly Gly Ser Glu Ser Glu Glu Gly Met Ser Gly
            260                 265                 270

Ser Glu Gly Gly Met Ser Gly Gly Gly Gly Ser Lys Ser Lys Ser Lys
        275                 280                 285

Lys Ser Lys Leu Lys Ala Lys Leu Gly Lys Lys Lys Gly Met Ser Gly
    290                 295                 300

Gly Met Ser Gly Ser Glu Glu Gly Met Ser Gly Ser Glu Gly Gly Met
305                 310                 315                 320

Ser Ser Gly Gly Gly Ser Lys Ser Lys Ser Lys Lys Ser Lys Leu Lys
                325                 330                 335

Ala Lys Leu Gly Lys Lys Lys Gly Met Ser Gly Gly Met Ser Gly Ser
            340                 345                 350

Glu Glu Gly Met Ser Gly Ser Glu Gly Gly Met Ser Gly Gly Gly Gly
        355                 360                 365

Gly Lys Ser Lys Ser Arg Lys Ser Lys Leu Lys Ala Lys Leu Gly Lys
    370                 375                 380

Lys Lys Cys Met Ser Gly Gly Met Ser Gly Ser Glu Gly Gly Met Ser
385                 390                 395                 400

Gly Ser Glu Gly Gly Ile Ser Gly Gly Gly Met Ser Gly Gly Ser Gly
                405                 410                 415

Ser Lys His Lys Ile Gly Gly Gly Lys His Gly Gly Leu Gly Gly Lys
            420                 425                 430

Phe Gly Lys Lys Arg Gly Met Ser Gly Ser Gly Gly Gly Met Ser Gly
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Ser Glu Gly Gly Val Ser Gly Ser Glu Gly Ser Met Ser Gly Gly Gly
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Gly Gly Leu Arg Gly Lys Phe Gly Lys Lys Arg Gly Met Ser Gly Ser
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Glu Gly Gly Met Ser Gly Ser Glu Gly Gly Met Ser Glu Ser Gly Met
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Phe Gly Gly Gly Lys His Gly Gly Gly Gly Gly His Met Ala Glu
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<220>
<223> Complete sequence of the promoter region of the AtGRP17

<400> 3

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attcaatcgt gagacattga aattgtcgtt tctccattac ctttttggaa gaaaaaccat      180

cgaaagctag ctaagacttt ttttattaaa cgaacttgct actatttcta tgttttcttt      240

gaaatgaaaa ttaaatttgt tactgtttca cctaaaactc aaaagtattg ctttttaatt      300

ttattattaa gaaaaactaa tcttatttat gttaagaaac ctgtcaattt ttcattgtta      360

atttcggctc tataattatt aattaacaat caatttctca aaaattgcaa tcatgattat      420

gattagatat atattagttg gattgtgatg cattttttgt aatataaaat ggatgtttgt      480

attagtttct cactcatgta attaaacacc aaatgctaga aactagtact tttgtttctc      540

agctctcgtc tattgttata tctgcaacac gaacaaaaac cttatctagg tgttatatat      600

cacggttatg tttatgagtt agaagggatt cttcaacaaa aatcacggaa ctacttgtat      660

atatgtatgt gtgtatccga tcgaggttga cttccggggt tggacgttga agaagacgaa      720

ttcattgatt gggcttatat atgggcatgt attacttggt tcaagtttgt aacactttta      780
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gctttttcaa ttctattcga aaccaaaata ttgggctata tatctttata caaccttcaa 840

gataaattgg accaatttta gaagagcaaa ttgaacccgg ccgttagcgt tagccaaacc 900

ccaactcctt ttcagtacaa ttaaatcaag aatttctaat aaatcgtgaa tttctagaca 960

tacatatcat aatttcgtca aagcgagcct acacctagtt ttgagctaca taactctttt 1020

ctttttttt ttatgattag gaggtttcaa aacccttgga cccataattt cttataatta 1080

gttttgtaat actaaattta ccattgagag cgacctctcg tcactagtaa ttcgaagatc 1140

tcatattcat gacctatatt aaccatcttc cagtcaagta atttcaatcg aaattcatca 1200

aaatcatata tttaacttag taatcacata tgatatggct aatatacgta atataacgat 1260

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cacacacgaa aagagaaaat ataaagaagg acatgtaacg tgacgtagcg tagatctcca 1440

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tcagaaaat 1569